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## A map of the cis-regulatory sequences in the mouse genome.

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Authors:	Y Shen, F Yue, D F McCleary, Z Ye, L Edsall, S Kuan, U Wagner, J Dixon, L Lee, V V Lobanenkov, B Ren
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### Public Summary:

The laboratory mouse is the most widely used mammalian model organism in biomedical research. The  $2.6 \times 10^9$  bases of the mouse genome possess a high degree of conservation with the human genome, so a thorough annotation of the mouse genome will be of significant value to understanding the function of the human genome. So far, most of the functional sequences in the mouse genome have yet to be found, and the cis-regulatory sequences in particular are still poorly annotated. Comparative genomics has been a powerful tool for the discovery of these sequences, but on its own it cannot resolve their temporal and spatial functions. Recently, ChIP-Seq has been developed to identify cis-regulatory elements in the genomes of several organisms including humans, *Drosophila melanogaster* and *Caenorhabditis elegans*. Here we apply the same experimental approach to a diverse set of 19 tissues and cell types in the mouse to produce a map of nearly 300,000 murine cis-regulatory sequences. The annotated sequences add up to 11% of the mouse genome, and include more than 70% of conserved non-coding sequences. We define tissue-specific enhancers and identify potential transcription factors regulating gene expression in each tissue or cell type. Finally, we show that much of the mouse genome is organized into domains of coordinately regulated enhancers and promoters. Our results provide a resource for the annotation of functional elements in the mammalian genome and for the study of mechanisms regulating tissue-specific gene expression.

### Scientific Abstract:

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